

In re Application of:
Frudakis and Shriver
Application No.: 10/644,594
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Attorney Docket No.: DNA1170-2

Amendments to the Claims

Please amend claims 1, 5, 6, 8, 24, 31 and 37, 39-43, 45, 48-51, 53, and 56 as indicated in the listing of claims.

Please cancel claims 4, 12, 15, 16, 21, and 22 without prejudice or disclaimer.

The listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claim 1. (Currently Amended) A method of inferring a trait of an individual, comprising:

a) contacting a sample comprising nucleic acid molecules of the individual with hybridizing oligonucleotides wherein the contacting detects detecting, in a nucleic acid sample from an individual, nucleotide occurrences of single nucleotide polymorphisms (SNPs) in a panel of at least about ten ancestry informative markers (AIMs), wherein the panel comprises at least about ten AIMS selected from SEQ ID NOS:1 to 331, wherein the nucleotide occurrences of the SNPs~~AIMs~~ are indicative of a population structure, wherein the population structure is correlated with ~~the~~ a trait of the individual, and wherein the panel comprises at least one AIM that is not linked to a gene linked to the trait, —; and

b) identifying the population structure indicated by the nucleotide occurrences of the SNPs~~AIMs~~ detected in the individual of step a), wherein identifying the population structure infers the trait,

~~thereby inferring, , the trait of the individual.~~

Claim 2. (Cancelled)

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Claim 3. (Original) The method of claim 1, wherein the trait comprises biogeographical ancestry (BGA).

Claim 4. (Cancelled)

Claim 5. (Currently Amended) The method of claim 3, wherein the panel comprises at least about ten AIMs set forth as selected from SEQ ID NOS:1 to 71.

Claim 6. (Currently Amended) The method of claim 3, wherein the panel comprises ~~AIMs set forth as~~:

SEQ ID NOS:7, 21, 23, 27, 45, 54, 59, 63, and 72 to 152;
SEQ ID NOS:3, 8, 9, 11, 12, 33, 40, 59, 63, and 153 to 239; or
SEQ ID NOS:1, 8, 11, 21, 24, 40, 172, and 240 to 331; or
combinations thereof.

Claim 7. (Cancelled)

Claim 8. (Currently Amended) The method of claim 3, wherein the BGA comprises a proportion of a sub-Saharan African, Native American, IndoEuropean, or East Asian ancestral group, or a combination of said-the ancestral groups.

Claim 9. (Original) The method of claim 8, wherein the BGA comprises a proportion of at least three ancestral groups.

Claims 10 to 23 (Cancelled)

Claim 24. (Currently Amended) The method of claim 1, further comprising identifying a sub-population structure of the population structure indicated by the nucleotide occurrences of the SNPs-AIMs detected in the individual in-of step a), wherein the sub-population structure infers with the trait.

Claims 25 to 28. (Cancelled)

Claim 29. (Original) The method of claim 1, which is performed in a high throughput format.

Claim 30. (Original) The method of claim 1, which is performed in a multiplex format.

Claim 31. (Currently Amended) A method of estimating proportional ancestry of at least two ancestral groups of an individual, comprising:

- a) contacting a sample comprising nucleic acid molecules of the individual with hybridizing oligonucleotides wherein the contacting detects detecting, in a nucleic acid sample from an individual, nucleotide occurrences of single nucleotide polymorphisms (SNPs) in a panel of at least about ten ancestry informative markers (AIMs), wherein the panel comprises at least about ten AIMs selected from SEQ ID NOS:1 to 331, wherein the nucleotide occurrences of the SNPs-AIMs are indicative of a population structure, wherein the population structure is correlated with biogeographical ancestry (BGA) for each of the at least two ancestral groups, and wherein the panel comprises at least one AIM that is not linked to a gene linked to BGA; and
- b) identifying the population structure indicated by the nucleotide occurrences of the SNPs-AIMs detected in the individual of step a), wherein identifying the population structure estimates proportional ancestry,
thereby estimating proportional ancestry of the individual.

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Claim 32. (Original) The method of claim 31, wherein the proportional ancestry comprises a proportion of a sub-Saharan African ancestral group, a Native American ancestral group, an IndoEuropean ancestral group, an East Asian ancestral group, or a combination thereof.

Claims 33 to 36. (Cancelled)

Claim 37. (Currently Amended) The method of claim 31, wherein the panel for at least one of the ancestral groups comprises ~~AIMs set forth as:~~

SEQ ID NOS:7, 21, 23, 27, 45, 54, 59, 63, and 72 to 152;
SEQ ID NOS:3, 8, 9, 11, 12, 33, 40, 59, 63, and 153 to 239; or
SEQ ID NOS:1, 8, 11, 21, 24, 40, 172, and 240 to 331; or
combinations thereof.

Claim 38. (Cancelled)

Claim 39. (Currently Amended) The method of claim 31, wherein the proportional ancestry comprises proportions of three ancestral groups, and

wherein identifying the population structure indicated by the nucleotide occurrences of the ~~SNPs~~ AIMs detected in of the individual of step a) comprises:

performing a likelihood determination for affiliation with each of a sub-Saharan African ancestral group, a Native American ancestral group, an IndoEuropean ancestral group, and an East Asian ancestral group;

thereafter selecting three ancestral groups having a greatest likelihood value;

determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure that correlates with

the nucleotide occurrences of the SNPs-the AIMs detected in of the individual of step a) is identified; and

identifying a single proportional combination of maximum likelihood, thereby estimating the proportional ancestry of the individual.

Claim 40. (Currently Amended) The method of claim 31, wherein the proportional ancestry comprises proportions of three ancestral groups, and wherein identifying a population structure indicated by the nucleotide occurrences of the SNPs-AIMs detected in the individual of step a) comprises:

performing six two-way comparisons comprising likelihood determinations for affiliation between each group with each other group;

thereafter selecting three ancestral groups having a greatest likelihood value;

determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure that correlates with the nucleotide occurrences of the SNPs-AIMs detected in the individual of step a) of the individual is identified; and

identifying a single proportional combination of maximum likelihood, thereby estimating the proportional ancestry of the individual.

Claim 41. (Currently Amended) The method of claim 31, wherein the proportional ancestry comprises proportions of three ancestral groups, and

wherein identifying the population structure indicated by the nucleotide occurrences of the SNPs-AIMs detected in of the individual of step a) comprises:

performing three three-way comparisons among the groups,

determining a likelihood of all possible proportional affiliations among the three ancestral groups having the greatest likelihood value, whereby a population structure that correlates with

the nucleotide occurrences of the SNPs-AIMs detected in of the individual of step a) is identified; and

identifying a single proportional combination of maximum likelihood, thereby estimating the proportional ancestry of the individual.

Claim 42. (Currently Amended) The method of claim 31, wherein the proportional ancestry comprises proportions of four ancestral groups, and

wherein identifying the population structure indicated by the nucleotide occurrences of the SNPs-AIMs detected in of the individual of step a) comprises performing six two-way comparisons, three three-way comparisons, or one four-way comparison among the four ancestral groups;

determining a likelihood of all possible proportional affiliations among the four ancestral groups having the greatest likelihood value, whereby a population structure that correlates with the nucleotide occurrences of the SNPs-AIMs detected in of the individual of step a) is identified; and

identifying a single proportional combination of maximum likelihood, thereby estimating the proportional ancestry of the individual.

Claim 43. (Currently Amended) The method of claim 40, further comprising generating a graphical representation of the comparison of the three ancestral groups, said the graphical representation comprising a triangle with each ancestral group independently represented by a vertex of the triangle, wherein the maximum likelihood value of proportional affiliation for an individual comprises a point within the triangle.

Claim 44. (Original) The method of claim 43, wherein the graphical representation further comprises a confidence contour indicating a level of confidence associated with estimating the proportional ancestry.

Claim 45. (Currently Amended) The method of claim 31, further comprising identifying an ethnicity of the individual, which comprises identifying a sub-population structure of the population structure indicated by the nucleotide occurrences of the AIMs detected in the test individual of step a), wherein the AIMs are further indicative of a sub-population structure, wherein the sub-population structure infers ethnicity of the ~~test~~-individual.

Claim 46. (Cancelled)

Claim 47. (Original) The method of claim 45, wherein the ancestral group is IndoEuropean, and wherein the ethnicity comprises Northern European or Mediterranean.

Claim 48. (Previously Presented) The method of claim 31, further comprising generating an ancestral map of the world, wherein locations of populations having a proportional ancestry corresponding to the proportional ancestry of the individual are indicated on the ancestral map.

Claim 49. (Currently Amended) The method of claim 48, further comprising

- overlays the ancestral map with a genealogical map, wherein the genealogical map indicates locations of populations having geopolitical relevance with respect to the ~~test~~ individual, and
- statistically combining the information of the ancestral map and genealogical map to obtain a most likely estimate of family history of the ~~test~~-individual.

Claim 50. (Currently Amended) The method of claim 31, wherein identifying a population structure indicated by the nucleotide occurrences of the SNPs-AIMs detected in the individual of step a) comprises comparing the nucleotide occurrences of the SNPsAIMS detected in of the individual of step a) with known proportional ancestries corresponding to nucleotide occurrences of SNPs-AIMs indicative of BGA.

Claim 51. (Currently Amended) The method of claim 50, wherein the known proportional ancestries corresponding to nucleotide occurrences of SNPs-AIMs indicative of BGA are contained in a database.

Claim 52. (Original) The method of claim 51, wherein the comparing is performed using a computer.

Claim 53. (Currently Amended) The method of claim 50, wherein each of the known proportional ancestries corresponding to nucleotide occurrences of SNPs-AIMs indicative of BGA further comprises at least one photograph of a person from whom the known proportional ancestry was determined.

Claim 54. (Previously Presented) The method of claim 53, wherein the at least one photograph comprises a digital photograph.

Claim 55. (Original) The method of claim 54, wherein digital information comprising the digital photograph is contained in a database.

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Claim 56. (Currently Amended) The method of claim 55, wherein the digital information in the database is associated with the known proportional ancestry corresponding to nucleotide occurrences of SNPs-AIMs indicative of BGA of the person in the photograph.

Claim 57. (Previously Presented) The method of claim 51, further comprising identifying at least one photograph of a person having a proportional ancestry corresponding to the proportional ancestry of the individual.

Claim 58. (Original) The method of claim 57, wherein identifying the photograph comprises scanning a database comprising a plurality of files, each file comprising digital information corresponding to a digital photograph of a person having a known proportional ancestry, and identifying at least one photograph of a person having nucleotide occurrences of AIMs indicative of BGA that correspond to the nucleotide occurrences of AIMs indicative of BGA of the ~~test~~ individual.

Claims 59-82 (Cancelled)